

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/689,343A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ✓ PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) 4. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

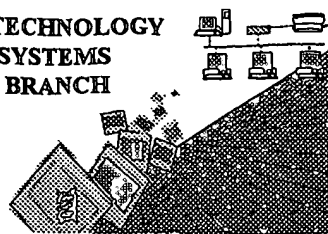
TECH CENTER 2900/2900

APR 25 2002

RECEIVED

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



TECH CENTER 1600/2900

APR 25 2002

RECEIVED

#7

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/689,343A
Source: 1600
Date Processed by STIC: 4/16/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



1636

RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/689,343A

TIME: 11:52:53

Input Set : A:\NEB-181.txt

Output Set: N:\CRF3\04162002\I689343A.raw

see Mr. 5-6

Does Not Comply
Corrected Diskette Needed

```

3 <110> APPLICANT: VAISVILA, ROMUALDAS
4   MORGAN, RICHARD D.
5   KUCERA, REBECCA B.
6   CLAUS, TOBY E.
7   RALEIGH, ELISABETH A.
9 <120> TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE MseI RESTRICTION
10  ENDONUCLEASE
12 <130> FILE REFERENCE: NEB-181
14 <140> CURRENT APPLICATION NUMBER: 09/689,343A
15 <141> CURRENT FILING DATE: 2000-10-12
17 <160> NUMBER OF SEQ ID NOS: 9
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 903
23 <212> TYPE: DNA
24 <213> ORGANISM: Micrococcus sp.
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(900)
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33   1           5           10           15
35 gag gcg gac aac ctc gat ttc att caa acg ctc ccc gac gcg agc ttc   96
36 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
37           20           25           30
39 cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg   144
40 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
41           35           40           45
43 ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc   192
44 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
45   50           55           60
47 ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat   240
48 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
49  65           70           75           80
51 gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg   288
52 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
53           85           90           95
55 gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg   336
56 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
57           100          105          110
59 gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc   384
60 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe

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Input Set : A:\NEB-181.txt

Output Set: N:\CRF3\04162002\I689343A.raw

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61          115          120          125
63 gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc 432
64 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
65          130          135          140
67 gcg cgc tcg aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg 480
68 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
69 145          150          155          160
71 tat gtg aag gac ccg aac tac gtc tgg aac ggt cag gat gta gat 528
72 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
73          165          170          175
75 cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg 576
76 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
77          180          185          190
79 ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct 624
80 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
81          195          200          205
83 gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc 672
84 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
85          210          215          220
87 atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg 720
88 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
89 225          230          235          240
91 gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc 768
92 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
93          245          250          255
95 gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta 816
96 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
97          260          265          270
99 atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc 864
100 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
101          275          280          285
103 gtg cag act ccc cag agt gac cca cga acc gac gga tga 903
104 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
105          290          295          300
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 300
110 <212> TYPE: PRT
111 <213> ORGANISM: Micrococcus sp.
113 <400> SEQUENCE: 2
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115 1 5 10 15
117 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
118 20 25 30
120 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
121 35 40 45
123 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
124 50 55 60
126 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
127 65 70 75 80

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Input Set : A:\NEB-181.txt

Output Set: N:\CRF3\04162002\I689343A.raw

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129 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
130      85      90      95
132 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
133      100      105      110
135 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
136      115      120      125
138 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
139      130      135      140
141 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
142 145      150      155      160
144 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
145      165      170      175
147 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
148      180      185      190
150 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
151      195      200      205
153 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
154      210      215      220
156 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
157 225      230      235      240
159 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
160      245      250      255
162 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
163      260      265      270
165 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
166      275      280      285
168 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
169      290      295      300
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173 <211> LENGTH: 1236
174 <212> TYPE: DNA
175 <213> ORGANISM: Unknown
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Unknown Organism: ENVIRONMENTAL DNA
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (1)..(1233)
184 <220> FEATURE:
185 <223> OTHER INFORMATION: At position 594, N = G, A, C or T
187 <400> SEQUENCE: 3
188 atg cct aca ctg gat tgg ccc ggt aaa cag tta agc ttc cca cca gct 48
189 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
190 1 5 10 15
192 acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg 96
193 Thr Ser Leu His Leu Glu Ser Val Thr Glu Gly Ala Glu Ser Pro
194 20 25 30
196 cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg 144
197 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
198 35 40 45

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Input Set : A:\NEB-181.txt

Output Set: N:\CRF3\04162002\I689343A.raw

200 ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct 192
 201 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
 202 50 55 60
 204 ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat 240
 205 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
 206 65 70 75 80
 208 tcg cgt cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag 288
 209 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
 210 85 90 95
 212 tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta 336
 213 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
 214 100 105 110
 216 ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg 384
 217 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
 218 115 120 125
 220 gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc 432
 221 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
 222 130 135 140
 224 ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc 480
 225 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
 226 145 150 155 160
 228 tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt 528
 229 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
 230 165 170 175
 232 tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa 576
 233 Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
 234 180 185 190
 W--> 236 cct tac cat ccg agc acn cat aag acc ttc gct tcc tcc ccg aag gcc 624
 237 Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
 238 195 200 205
 240 ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac 672
 241 Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
 242 210 215 220
 244 tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc 720
 245 Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
 246 225 230 235 240
 249 tat ccg act caa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc 768
 250 Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
 251 245 250 255
 253 tcc tcg aac gca ggc gat ctg gtg gca gac ttc ttc tgc ggc tca ggg 816
 254 Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
 255 260 265 270
 257 aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac 864
 258 Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
 259 275 280 285
 261 gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc 912
 262 Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
 263 290 295 300
 265 gag gga gta agt ttc act ttt gaa cgc cag gaa act ttt act cta cct 960

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266 Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
267 305 310 315 320
269 atc cag cca ctt cca cca gat tgg ttg atc atc gcc gag gag cag att 1008
270 Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
271 325 330 335
273 cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gtg gac gat caa 1056
274 Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
275 340 345 350
277 tgg gat ggc aaa atc ttc cgc agc cgt cat caa ggc tta cgc tcc cgc 1104
278 Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
279 355 360 365
281 ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg 1152
282 Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
283 370 375 380
285 ttg tgt gta cgg gta gtg agc cgt gaa ggg gaa tac tat gag ttc aca 1200
286 Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
287 385 390 395 400
289 ggt cga gcc gat agc cct cac ccc gta tcg ttt tga 1236
290 Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
291 405 410
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 411
296 <212> TYPE: PRT
297 <213> ORGANISM: Unknown
299 <220> FEATURE:
300 <223> OTHER INFORMATION: At position 198, Xaa = any amino acid
302 <400> SEQUENCE: 4
303 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
304 1 5 10 15
306 Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
307 20 25 30
309 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
310 35 40 45
312 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
313 50 55 60
315 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
316 65 70 75 80
318 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
319 85 90 95
321 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
322 100 105 110
324 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
325 115 120 125
327 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
328 130 135 140
330 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
331 145 150 155 160
333 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
334 165 170 175

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see item 6 on Error Summary Sheet

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/689,343A

DATE: 04/16/2002
TIME: 11:52:54

Input Set : A:\NEB-181.txt
Output Set: N:\CRF3\04162002\I689343A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 594
Seq#:3; Xaa Pos. 198
Seq#:4; Xaa Pos. 198

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:6

another error